engaging the subject in extensive exercise training for a period of time sufficient to improve the cholesterol levels in the subject.

4. A method of improving diabetes status in a subject in need of such improvement, the method comprising:

identifying a subject with diabetes or at risk of developing diabetes having an "11" genotype for the second exon of the myostatin gene, wherein the subject is in need of improved diabetes status; and

engaging the subject in extensive exercise training for a period of time sufficient to improve the diabetes status in the subject.

IN THE SPECIFICATION:

Please delete the paragraph on page 6, lines 28-30 thru page 7, lines 1-9, and replace it with the following paragraph:

Genotyping for the (C581T) and (A30G) substitutions in GLUT4 was performed by amplification using sense primer 5'-CAGTGCCCGGAGCAGGGAGGCGCT-3' (SEQ ID NO: 1) and antisense primer 5'-GCGAAGATGAAAGAACCGATCCTG-3' (SEQ ID NO: 2) followed by digestion with the restriction endonucleases AvaII and BamHI, respectively. The presence of a C at np-518 yields major AvaII restriction fragments of 408 and 378 base pairs and the presence of a T at np-518 yields fragments of119, 289 and 378 base pairs. The presence of an A at np-30 yields major BamHI fragments of 389 and 342 base pairs, while the presence of a G at np-30 yields fragments of 445 and

389 base pairs. All denotations of sequence positions are based on those recited in Bjorbaek et al. (1994), *Diabetes*, 43:976-983, hereby incorporated by reference.

Please delete the paragraph on page 7, lines 12-23, and replace it with the following paragraph:

DNA amplification primers for exon 2 of the human myostatin gene were designed based on the cDNA sequence of human myostatin (GenBank Accession No. AF019627) and the genomic organization of the bovine myostatin gene (Grobert et al. (1998), *Mamm. Gen.* 9:210-213, incorporated by reference. Amplimers were sequenced directly using the dRhodamine ready reaction kit (Perkin Elmer) and analyzed on the ABI Prism Model 377 (Applied Biosystems) fluorescent sequencer. Sequences were aligned for comparison using SEQUENCHER™ 3.0 (Gene Codes). Primer 1 had the sequence 5'-GAAAACCCAAATGTTGCTTC-3' (SEQ ID NO: 3), and primer 2 had the sequence 5'-TGTCTAGCTTATGAGCTTAGGG-3' (SEQ ID NO: 4). The temperature was 54°C, and the buffer was 2.0 mM MgCl. PCR products were digested with BanII and the digested products were run on 2% agarose gels.

Please delete the paragraph on page 7, lines 26-30 thru page 8, lines 1-3, and replace it with the following paragraph:

A 220 bp region encompassing the Gly972Arg substitution was amplified from approximately 20ng of genomic DNA with upstream primer 5'-GCAGCCTGGCAGGAGAGCCAT-3' (SEQ ID NO: 5) and downstream primer 5'-CTCACCTCCTCTGCAGCAATG-3' (SEQ ID NO: 6). PCR products were digested with